

Attorney Docket: 1874/120

SYNTHETIC PEPTIDES AND METHODS OF USE FOR AUTOIMMUNE DISEASE  
THERAPIES

Related Application

5 This application claims priority from provisional applications 60/093,859 filed July 23, 1998, and 60/123,675 filed March 9, 1999, both of which are hereby incorporated by reference herein.

Government Funding

10 This invention was made in part with government support under grant CA47554 awarded by the National Institutes of Health. The government has certain rights in the invention.

Background

15 An autoimmune disease results from an inappropriate immune response directed against a self antigen (an autoantigen), which is a deviation from the normal state of self-tolerance. Self-tolerance arises when the production of T cells and B cells capable of reacting against autoantigens has been prevented by events that occur in the development of the immune system during early life. The cell surface proteins that play a central role in regulation of immune responses through their ability to bind and present processed peptides to T cells are the major histocompatibility complex (MHC) molecules (Rothbard, J. B., et al., 1991, *Annu. Rev. Immunol.* 9:527).

20 A number of therapeutic agents have been developed to treat autoimmune diseases, including general anti-inflammatory drugs such as "super aspirins", for example, agents that can prevent formation of low molecular weight inflammatory compounds by inhibiting a cyclooxygenase; agents that can function by inhibiting a protein mediator of inflammation, for example, by sequestering the inflammatory protein tumor necrosis factor (TNF) with an anti-TNF specific monoclonal antibody or antibody fragment, or with a soluble form of the TNF receptor; agents that target a protein on the surface of a T cell and generally prevent interaction with an antigen presenting cell (APC) by inhibiting the CD4 receptor or the cell adhesion receptor ICAM-1. However, compositions having natural folded proteins as

therapeutic agents can incur problems in production, formulation, storage, and delivery. Several of these problems necessitate delivery to the patient in a hospital setting.

An additional target for inhibition of an autoimmune response is the set of lymphocyte surface proteins MHC molecules, particularly a protein encoded by an MHC class II gene, for example, HLA-DR, -DQ and -DP. Each of the MHC genes is found in a large number of alternative or allelic forms within a mammalian population. The genomes of subjects affected with certain autoimmune diseases, for example multiple sclerosis (MS) and rheumatoid arthritis (RA), are more likely to carry one or more characteristic MHC class II alleles, to which that disease is linked.

10 RA is a common human autoimmune disease with a prevalence of about 1% among Caucasians (Harris, E. J. et al., 1997, *In Textbook of Rheumatology* 898-932), currently affecting 2.5 million Americans. RA is characterized by chronic inflammation of the synovial joints and infiltration by activated T cells, macrophages and plasma cells, leading to a progressive destruction of the articular cartilage. It is the most severe form of joint disease. 15 Inherited susceptibility to RA is strongly associated with the affected subject having at the MHC class II DRB1 locus the allele DRB1\*0401, DRB1\*0404, or DRB1\*0405 or the DRB1\*0101 allele. The nature of the autoantigen(s) in RA is poorly understood, although collagen type II (CII) is a prominent candidate. An immunodominant T cell epitope in collagen type II corresponding to residues 261-273 has been identified (Fugger, L., et al., 20 1996, *Eur. J. Immunol.* 26: 928-933).

It would be desirable to identify agents that were able to bind specifically to one or more of the linked MHC class II molecules and thereby to inhibit an inappropriate immune response. An agent that interacts and binds relatively nonspecifically to several MHC class II molecules is Copolymer 1 (Cop 1), a synthetic amino acid heteropolymer that was shown to 25 be capable of suppressing experimental allergic encephalomyelitis (EAE; Sela, M., R. Arnon, et al., 1990, *Bull. Inst. Pasteur* (Paris)), which can be induced in the mouse and is a model for MS. Cop 1 which is poly(Y,E,A,K), indicated herein "YEAKE" using the one letter amino acid code (see infra; Y represents tyrosine, E glutamic acid, A alanine, and K lysine) has been used to treat relapsing forms of MS but does not suppress the disease entirely

(Bornstein, M. B., et al., 1987, *N. Engl. J. Med.* 317:408; Johnson, K P., et al., 1995, *Neurology* 45:1268). There is no suggestion that YEAK is an effective treatment for another autoimmune disease such as RA.

There is a need for improved treatments for autoimmune diseases. A potential source  
5 of such treatments would be to identify agents that bind selectively to a purified MHC class II  
allele protein molecule in vitro, particularly to a protein which is a product of an MHC class  
II allele that is associated with an autoimmune disease. In addition, the agent should also  
bind to that protein as it occurs on the surfaces of antigen presenting cells in vivo, and  
thereby can block, anergize, or inactivate T cells that are responsible for the autoimmune  
10 disease.

#### Brief Description of the Drawings

Fig. 1 shows inhibition of binding of biotinylated heteropolymer molecules to  
recombinant empty soluble MHC class II purified proteins by different competitors. Fig. 1A  
shows inhibition of binding to recombinant HLA-DR1 protein, and Fig. 1B shows inhibition  
15 of binding to recombinant HLA-DR4 protein. Concentrations of unlabeled competitors  
(heteropolymers, influenza virus hemagglutinin (HA) peptide 306-318, or type II collagen  
(CII) peptide 261-273), are indicated on the abscissa. In each panel, inhibition by CII 261-  
273 is shown as open circles, inhibition by HA 306-318 is shown by solid circles, inhibition  
by the three-amino acid heteropolymer indicated is shown by open or solid triangles, and  
20 inhibition by YEAK is shown by solid squares. Specific binding observed and shown on the  
ordinate was calculated as percentage of inhibition using the formula: percentage of  
inhibition =  $100\% - [( \text{signal with competitor} - \text{background} ) / ( \text{signal without competitor} - \text{background} ) \times 100]$ .

Fig. 2 shows inhibition of IL-2 production by DR1-restricted CII -specific T cell  
25 hybridomas in the presence of different heteropolymers. Irradiated L57.23 cells (fibroblasts  
transfected with a gene encoding HLA-DR1) were coincubated in duplicate with collagen  
peptide CII 261-273 (40 µg/ml) and varying concentrations, shown on the abscissa, of  
heteropolymers for 2 hr at 37°C, then T cells (clone 3.19 or 19.3 as indicated) were added,  
and the mixtures were further incubated for 24 hr at 37°C. Supernatants (30 µl) were then

removed, and were assayed for activation as measured by IL-2 production as indicated by proliferation of IL-2-dependent cytotoxic T lymphocytes (CTL-L) as described in Example 2. Extent of inhibition by YAK is shown as solid circles, by YEA as solid triangles, by YEK as open triangles, and by YEAK (Cop 1) as solid squares. Percent inhibition of CTL-L proliferation shown on the ordinate was calculated using the formula: percentage of inhibition = 100% - [(signal with competitor - background)/(signal without competitor - background) x 100].

Fig. 3 shows inhibition of IL-2 production by DR4-restricted CII-specific T cell hybridomas (3838 and D3) in the presence of different heteropolymers. Fig. 3A shows the effects of coincubating irradiated 3838 or D3 Priess cells, and Fig. 3B shows the effects of incubating L cells transfected with a gene encoding HLA-DR4 with collagen peptide CII 261-273 at the fixed concentration of 40 µg/ml, and with varying concentrations of each of the heteropolymers, as indicated on the abscissa using the same symbols as in Fig. 2, in duplicate for 2 hr at 37°C. T cells were then added (clones 3838 or D3 as indicated) and samples were further incubated for 24 hr at 37°C, and were assayed as described in Fig. 2. All assays were conducted in duplicate.

#### Summary

In one embodiment of the invention, a composition is provided which is a synthetic peptide having an amino acid sequence comprising at least three residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids, the synthetic peptide being at least seven amino acid residues in length and capable of binding to an MHC class II protein associated with an autoimmune disease. Thus the aromatic amino acid is selected from the group consisting of tyrosine (Y), valine (V), and phenylalanine (F), the positively charged amino acid is lysine (K), and the sequence is selected from the group consisting of lysine-tyrosine (KY), lysine-valine (KV), and lysine-phenylalanine (KF). Further, the embodiment of the invention provides a composition wherein the negatively charged amino acid is glutamic acid (E), and the sequence is selected from the group consisting of glutamic acid-lysine-tyrosine (EKY), glutamic acid-lysine-valine (EKV), and glutamic acid-lysine-

phenylalanine (EKF). Even further, in the provided composition the amino acid which is aliphatic is alanine (A), and the sequence is selected from the group of amino acid sequences consisting of glutamic acid-lysine-tyrosine-alanine (EKYA), glutamic acid-lysine-valine-alanine (EKVA), and glutamic acid-lysine-phenylalanine-alanine (EKFA). The composition  
5 can further comprise an amino-terminal alanine, and the sequence is selected from the group of amino acid sequences consisting of alanine-glutamic acid-lysine-tyrosine-alanine (AEKYA), alanine-glutamic acid-lysine-valine-alanine (AEKVA), and alanine-glutamic acid-lysine-phenylalanine-alanine (AEKFA). The synthetic peptides that are the embodiments of the invention are capable of binding to an MHC class II protein associated  
10 with an autoimmune disease, for example, an arthritic condition, for example, rheumatoid arthritis. In another embodiment, the synthetic peptide composition which is an embodiment of the invention has aliphatic amino acid which is alanine, and the amino acid sequence is selected from the group of sequences consisting of: lysine-glutamic acid-tyrosine-alanine (KEYA), lysine-tyrosine-alanine-glutamic acid (KYAE), lysine-glutamic acid-valine-alanine  
15 (KEVA), lysine-valine-alanine-glutamic acid (KVAE), lysine-glutamic acid-phenylalanine-alanine (KEFA), and lysine-phenylalanine-alanine-glutamic acid (KFAE). In a further embodiment wherein the aliphatic amino acid is alanine (A), the amino acid sequence is selected from the group of amino acid sequences consisting of lysine-tyrosine-alanine-alanine (KYAA) or lysine-lysine-tyrosine-alanine (KKYA), lysine-valine-alanine-alanine (KVAA)  
20 or lysine-lysine-valine-alanine (KKVA), lysine-phenylalanine-alanine-alanine (KFAA), and lysine-lysine-phenylalanine-alanine (KKFA). In this embodiment, the peptide can further comprise two alanine residues, and the sequence can be selected from the group of sequences consisting of alanine-lysine-tyrosine-alanine-glutamic acid (AKYAE), glutamic acid-alanine-lysine-tyrosine-alanine (EAKYA), alanine-lysine-valine-alanine-glutamic acid (AKVAE);  
25 and glutamic acid-alanine-lysine-valine-alanine (EAKVA), and alanine-lysine-phenylalanine-alanine-glutamic acid (AKFAE); and glutamic acid-alanine-lysine-phenylalanine-alanine (EAKFA). The peptide composition of this embodiment of the invention can be 7-100 amino acid residues in length.

Another embodiment of the invention provides a composition which is a synthetic

peptide having therapeutic activity in a subject suffering from an autoimmune disease, and the amino acid sequence having at least one of each of amino acids glutamic acid, lysine, and alanine and an amino acid selected from the group consisting of tyrosine, valine, and phenylalanine. The composition can be a peptide which is 7-100 amino acids in length, for example, 7-50 amino acids in length, 7-25 amino acids in length, and 7-15 amino acids in length. The composition can be formulated as a unitary dosage in a pharmaceutically acceptable carrier, for example, a synthetic peptide which is substantially pure. An embodiment of the invention is a synthetic peptide having greater affinity for the antigen binding groove of an MHC class II protein associated with the autoimmune disease than a type II collagen 261-273 peptide. In a further example of these embodiments, a composition is provided comprising an amino acid analog at the residue locations and in an amount protease degradation of the peptide in the subject.

Another embodiment of the invention is an isolated peptide composition having a sequence selected from the group consisting of: AKEYAAAAAAKAAAA (SEQ ID NO: 7),  
15 AA EYAAAAAAKAAAA (SEQ ID NO: 12), AAKYAEAAAAKAAAA (SEQ ID NO: 15),  
and EAKYAAAAAAKAAAA (SEQ ID NO: 18). A further embodiment of the invention is an example of one of the preceding isolated peptides in which the tyrosine (Y) has been substituted by a valine (F) or a phenylalanine (F). Further, an embodiment of the invention can be an isolated peptide composition having a sequence selected from the group consisting  
20 of: AEKYAAAAAAKAAAA (SEQ ID NO: 6), AKEYAAAAAAKAAAA (SEQ ID NO: 7),  
K EAYAAAAAAKAAAA (SEQ ID NO: 10), AEEYAAAAAAKAAAA (SEQ ID NO: 11),  
AA EYAAAAAAKAAAA (SEQ ID NO: 12), EKAYAAAAAAKAAAA (SEQ ID NO: 13),  
AAKY EAAAAKAAAA (SEQ ID NO: 14), AAKYAEAAAAKAAAA (SEQ ID NO: 15),  
EAA YAAAAAAKAAAA (SEQ ID NO: 16), EKKYAAAAAAKAAAA (SEQ ID NO: 17),  
25 EAKYAAAAAAKAAAA (SEQ ID NO: 18), AKKY EAAAAA AAAAA (SEQ ID NO: 21),  
AA EYKAAAAA AAAAA (SEQ ID NO: 26), AAKY EAAAAA AAAAA (SEQ ID NO: 28),  
AAKYAEAAAAA AAAAA (SEQ ID NO: 29), AEYAKAAAAA AAAAA (SEQ ID NO: 32),  
AEKYAAAAA AAAAA (SEQ ID NO: 33), AYKAEAAAAA AAAAA (SEQ ID NO: 35),  
and AKYAEAAAAA AAAAA (SEQ ID NO: 36), the peptide having high affinity for an

MHC class II protein. Yet another embodiment of the invention is an isolated peptide according to any of the preceding sequences in which the tyrosine (Y) has been substituted by a valine (F) or a phenylalanine (F).

Another embodiment of the invention provides an isolated peptide composition having  
5 an amino acid sequence capable of inhibiting immune response in a subject to an autoantigen, wherein a position in the amino acid sequence of the peptide that corresponds to an antigen binding pocket in a peptide binding groove of an MHC class II DR protein is identified as a particular amino acid. For example, an isolated peptide composition is provided wherein the autoantigen is associated with a condition selected from the group consisting of multiple  
10 sclerosis and arthritis. The MHC class II protein can be selected from the group consisting of an HLA-DR1 protein, an HLA-DR4 protein. In another embodiment, the MHC class II protein is MHC class II HLA-DR2. An embodiment of the invention provides an isolated peptide, wherein the amino acid residue in the position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is selected from the group  
15 consisting of a tyrosine, a valine, and a phenylalanine. This embodiment further provides an isolated peptide composition wherein the amino acid residue in a first amino acid position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is alanine. The embodiment further provides an isolated peptide composition, wherein the amino acid residue located eight residues beyond the first amino acid position of the sequence  
20 that corresponds to the P1 pocket in the MHC class II peptide binding groove is selected from the group consisting of lysine and alanine residues, and the amino acid residue that corresponds to the P1 pocket is selected from the group consisting of tyrosine, valine, and phenylalanine.

Another example of this invention provides a pharmaceutical preparation comprising a  
25 first peptide sequence and a second peptide sequence, wherein the composition is a mixture of first peptide sequence and the second peptide sequence, the first sequence having a lysine residue and the second sequence having an alanine residue at the amino acid position corresponding to eight residues beyond the amino acid corresponding to the P1 pocket in the MHC class II peptide binding groove.

The autoimmune disease is selected from the group consisting of: multiple sclerosis, myasthenia gravis, Hashimoto's disease, systemic lupus erythematosus, uveitis, Guillain-Barre' syndrome, Grave's disease, idiopathic myxedema, autoimmune oophoritis, chronic immune thrombocytopenic purpura, colitis, diabetes, psoriasis, pemphigus vulgaris, and  
5 rheumatoid arthritis. In particular, the therapeutic composition embodiment of the invention can be used to treat an autoimmune disease which is an arthritic condition. Further, the therapeutic composition embodiment of the invention can be used to treat an autoimmune disease which is a demyelinating disease. In yet another embodiment, the therapeutic composition embodiment of the invention can be used to treat an autoimmune disease which  
10 is an inflammatory disease. For example, an embodiment of the invention is a therapeutic composition to treat the autoimmune disease rheumatoid arthritis. In another example, an embodiment of the invention is a therapeutic composition to treat the autoimmune disease multiple sclerosis.

In another embodiment of the invention, a method is provided for obtaining an MHC  
15 class II amino acid binding motif sequence in a mixture of synthetic peptide heteropolymers having therapeutic activity in a subject, comprising the steps of : (a) binding the mixture of synthetic heteropolymers to MHC class II protein molecules to form a heteropolymer-MHC protein complexes; (b) removing by peptidase enzyme digestion the amino terminal amino acid residues of the heteropolymers protruding from the heteropolymer-MHC protein  
20 complex to align amino termini of the heteropolymers to the edge of the MHC protein complexes; and (c) eluting the aligned heteropolymers from the MHC protein by dissociating the complexes to release the amino terminal aligned heteropolymers having the binding motif. In this method an additional step (d) can comprise: determining the amino terminal sequence of the aligned heteropolymers to obtain the binding motif. Further, in this method  
25 an additional an additional step (e) can comprises: comparing the amino terminal sequence of the aligned heteropolymers to the amino acid sequence of the synthetic heteropolymer composition. In this method, the MHC class II protein is associated with an autoimmune disease, for example, the autoimmune disease is an arthritic condition or a demyelinating condition.



In another embodiment of this method, an additional step (e) can comprise: synthesizing a plurality of peptide preparations, each peptide preparation having an amino acid sequence of a binding motif. In a further aspect of this method, an additional step (f) comprises: determining the affinity of each of the synthesized peptides for the MHC class II protein.

#### Detailed Description of Specific Embodiments

Unless the context otherwise requires, as used in this description and in the following claims, the terms below shall have the meanings as set forth:

The term "autoimmune condition" means a disease state caused by an inappropriate immune response that is directed to a self-encoded entity which is known as an autoantigen.

The term "derivative" of an amino acid means a chemically related form of that amino acid having an additional substituent, for example, N-carboxyanhydride group, a  $\gamma$ -benzyl group, an  $\epsilon$ ,N-trifluoroacetyl group, or a halide group attached to an atom of the amino acid.

The term "analog" means a chemically related form of that amino acid having a different configuration, for example, an isomer, or a D-configuration rather than an L-configuration, or an organic molecule with the approximate size and shape of the amino acid, or an amino acid with modification to the atoms that are involved in the peptide bond, so as to be protease resistant when polymerized in a peptide or polypeptide.

The phrases "amino acid" and "amino acid sequence" can include one or more components which are amino acid derivatives and/or amino acid analogs comprising part or the entirety of the residues for any one or more of the 20 naturally occurring amino acids indicated by that sequence. For example in an amino acid sequence having one or more tyrosine residues, a portion of one or more of those residues can be substituted with homotyrosine. Further, an amino acid sequence having one or more non-peptide or peptidomimetic bonds between two adjacent residues, is included within this definition.

The term "hydrophobic" amino acid means aliphatic amino acids alanine (A, or ala), glycine (G, or gly), isoleucine (I, or ile), leucine (L, or leu), proline (P, or pro), and valine (V, or val), the terms in parentheses being the one letter and three letter standard code abbreviations for each amino acid, and aromatic amino acids tryptophan (W, or trp),

phenylalanine (F, or phe), and tyrosine (Y, or tyr). These amino acids confer hydrophobicity as a function of the length of aliphatic and size of aromatic side chains, when found as residues within a protein.

5 The term "charged" amino acid means amino acids aspartic acid (D or asp), glutamic acid (E or glu), histidine (H or his), arginine (R or arg) and lysine (K or lys), which confer a positive (his, lys, and arg) or negative (asp, gly) charge at physiological values of pH in aqueous solutions on proteins containing these residues.

The term "anergy" means unresponsiveness of the immune system of a subject to an antigen.

10 The term "subject" as used herein indicates a mammal.

The term "arthritis condition" means at least one symptom of rheumatoid arthritis found in at least a single joint of a subject having the condition, for example in a shoulder, knee, hip or a digit of the subject. Examples of arthritis conditions include "polyarthritis", which is an arthritis condition that affects more than a single joint; "juvenile arthritis", an  
15 arthritis condition of a subject under the age of 21; and Felty's syndrome, which includes along with symptoms of rheumatoid arthritis (RA) also the symptoms of neutropenia, splenomegaly, weight loss, anemia, lymphadenopathy, and pigment spots on the skin.

The term "heterologous cell" means a cell for production of an MHC protein which is unrelated to a cell of a subject, i.e., the heterologous cell is not a cell of a mammal.

20 Preferably the heterologous cell is not from a warm blooded animal, even more preferably the heterologous cell is not from a vertebrate; in the most preferred embodiment the heterologous cell is an insect cell, or a cell of a microorganism such as a yeast cell.

The term "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antimicrobials such as antibacterial and antifungal agents,  
25 isotonic and absorption delaying agents and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, oral, intraperitoneal, transdermal, or subcutaneous administration, and the active compound can be coated in a material to protect it from inactivation by the action of acids or other adverse natural conditions.

Heteropolymers of Amino Acids as Therapeutic Agents for Autoimmune Diseases

This invention is directed to methods of use of a class of agents that can bind to specific MHC class II proteins. Such agent can bind to a class II protein, and thus inhibit and/or prevent the binding of an autoantigen involved in an autoimmune disease, or upon  
5 binding can induce anergy, so that there is no response of the immune system to the autoantigen.

The Class II MHC protein consists of two approximately equal-sized subunits,  $\alpha$  and  $\beta$ , which are transmembrane proteins. A peptide-binding cleft, which is formed by protein features from the amino termini of both  $\alpha$  and  $\beta$  subunits, is the site of presentation of the  
10 antigen to T cells. There are at least three types of Class II MHC molecules: HLA-DR, -DQ, and -DP, and there are numerous alleles of each type. The Class II MHC molecules are expressed predominantly on the surfaces of B lymphocytes and antigen presenting cells such as macrophages (Mengle-Gaw, L., *The Major Histocompatibility Complex (MHC)*, in the Encyclopedia of Molecular Biology, Oxford: Blackwell Science Ltd., 1994, pp. 602-606).

15 An embodiment of the invention includes a novel method for treating autoimmune diseases, by targeting MHC class II molecules with a class of compounds identified as heteropolymers that include three or more different amino acids. Further, the three amino acid heteropolymers are preferentially synthesized from those amino acids which are either charged or hydrophobic. Preferred charged amino acids are lysine and glutamic acid;  
20 preferred hydrophobic amino acids can be aromatic, for example, tyrosine or phenylalanine; and can be aliphatic, for example, alanine, valine, leucine, and isoleucine. Heteropolymers can be synthesized to a product of suitable molecular weight, in which the molecules can have a range of average molecular weights, for example, 2,000 daltons to 4,000 daltons; 3,000 daltons to 6,000 daltons; 5,000 daltons to 10,000 daltons; 8,000 daltons to 12,000  
25 daltons; and can extend to 20,000 daltons.

In another embodiment, a heteropolymer of the invention can be synthesized using f-moc or t-boc initiating amino acid analogs, or the like, which are immobilized on a resin in an automated peptide synthesis apparatus for further polymerization (solid state synthesis), yielding a heteropolymer product having a narrow range of molecular weights within the

polymer product population. In this embodiment, the average molecular weight of the product heteropolymer can be within 100 daltons of that of the longest and shortest molecule; within 200 daltons of that of the longest and shortest molecule; within 300 daltons of that of the longest and shortest molecule; within 400 daltons of that of the longest and shortest molecule; or within 800 daltons of that of the longest and shortest molecule within the population.

The amino acids are polymerized in molar ratios that can be adjusted to provide a heteropolymer with optimal binding characteristics, for example in YAK, having a molar ratio of at least three moles of lysine per mole of tyrosine in the final product, and at least four moles of alanine per mole of tyrosine in the final product. A preferred embodiment of a molar ratio for YAK is lysine:alanine:tyrosine in the proportions of 3.7:4.8:1.0. Another preferred embodiment of a molar ratio for YAK is lysine:alanine:tyrosine in the proportions of 3.1:4.3:1.0. A preferred embodiment of a molar ratio for YEK is lysine:glutamic acid:tyrosine in the proportions of 3.7:1.5:1.0. Another preferred embodiment of a molar ratio for YEK is lysine:glutamic acid:tyrosine in the proportions of 3.0:1.0:1.0. Other examples of three amino acid heteropolymers include poly(E,A,K) indicated EAK herein, a heteropolymer of glutamic acid, alanine, and lysine, and YEA described supra, and embodiments of preferred molar ratios for each, are shown in Table 1.

Synthesis procedures can include providing a solution which is a mixture of the chosen amino acids in an activated form, for example, activated as an N-carboxy anhydride, in the appropriate molar ratios of each of the appropriately derivatized amino acid precursors (derivatized to protect certain functional groups, such as the  $\epsilon$  amino group of L-lysine, for example the precursor  $\epsilon$ ,N-trifluoroacetyl-L-lysine). Alternatively, the synthesis procedure can involve online mixing during the synthetic procedure of derivatized precursors of the selected amino acids in the preferred molar ratios. Heteropolymer synthesis services can be obtained commercially, for example, at the Harvard Medical School Biopolymer Laboratory, Boston, MA, and at Advanced ChemTech, Inc., Louisville, KY. See the Advanced ChemTech 1998-1999 Product Catalog, which is herein incorporated by reference.

An embodiment of the invention is a method of use of a therapeutic heteropolymer

which includes a step of identifying the heteropolymer by its ability to inhibit binding of an antigenic peptide to an MHC class II molecule. In this embodiment, the MHC class II molecule is encoded by an HLA-DR1 or a -DR4 allele associated in the human population with subjects having an autoimmune disease, for example, RA, and the antigenic peptide is  
5 an immunodominant peptide obtained from the protein sequence of a sensitizing protein, for example, an epitope from collagen II (CII), for example, CII 261-273.

The heteropolymer compositions can be synthesized in solution using, for example, anhydride chemistry with appropriate derivatives of the selected amino acids. In another preferred embodiment, the heteropolymer compositions of the invention can be synthesized  
10 in a solid state system using a bead having a functionalized resin support. In a preferred embodiment, the heteropolymer is synthesized by solid state chemistry, using technologies that are known to one of skill in the art of amino acid heteropolymer synthesis. Such synthesis can be achieved for example using the Model 90 Tabletop Synthesizer (Advanced ChemTech, Louisville, KY) or an equivalent synthesizer available from Applied BioSystems  
15 (Foster City, CA).

Examples of such resin supports for peptide synthesis include a Merrifield resin, chloromethylated polystyrene with 1% DVB cross-links; an f-moc amino acid Wang resin, 4-benzyloxybenzyl alcohol, the resins being pre-loaded with an amino acid (for example, f-moc-D-trp(boc)-Wang resin). Resins are available in different mesh sizes, for example 100-  
20 200 mesh, and high loading or low loading densities of functionalization of the initiating amino acid.

A solution of the different derivatized amino acids to be polymerized into the composition of the invention, preferably protected as conventional in peptide synthesis, is added to sample of beads e.g., f-moc. Reagents for synthesis, for deblocking, and for  
25 cleavage of the complete heteropolymer molecules for removal from the resin are available from manufacturers of the apparatus (Applied Biosystems Peptide Synthesizer, Foster City, CA, or Advanced ChemTech, Louisville, KY); see e.g., M. Bodansky, *Principles of Peptide Synthesis*, 2nd Ed., Springer-Verlag, 1991, the contents of which are herein incorporated by reference. Additional amino acids or analogs or derivatives of amino acids, can be added to

the at least three amino acids selected to comprise the heteropolymers, to substitute for a small proportion of those amino acids, to provide, for example, a heteropolymer having increased protease resistance and therefore having enhanced pharmacological properties such as longer in vivo lifetime. Examples of analogs are homotyrosine, or other substituted  
5 tyrosine derivatives, and aminobutyric acid, each available as an f-moc derivative from Advanced ChemTech.

#### Therapeutic Compositions in the Methods of the Invention

The methods of the invention include incorporation of a heteropolymer into a pharmaceutical composition suitable for administration to a subject. In a preferred  
10 embodiment, the pharmaceutical composition includes an amino acid heteropolymer, for example, YAK, which is a heteropolymer of tyrosine, alanine, and lysine, in a pharmaceutically acceptable carrier. In another preferred embodiment, the pharmaceutical composition includes an amino acid heteropolymer, for example, YAK, which is a heteropolymer of tyrosine, alanine, and lysine, in a pharmaceutically acceptable carrier, in  
15 combination with another therapeutic agent. In another preferred embodiment, the pharmaceutical composition includes an oligopeptide of defined sequence, for example, a peptide of length 9-20 residues, comprising the amino acid sequence glutamic acid-lysine-tyrosine (EKY).

A composition of the present invention can be administered by a variety of other  
20 methods known in the art as will be appreciated by the skilled artisan. The active compound can be prepared with carriers that will protect it against rapid release, such as a controlled release formulation, including implants, transdermal patches, microencapsulated delivery systems. Many methods for the preparation of such formulations are patented and are generally known to those skilled in the art. See, e.g., *Sustained and Controlled Release Drug*  
25 *Delivery Systems*, J.R. Robinson, Ed., Marcel Dekker, Inc., NY, 1978. Therapeutic compositions for delivery in a pharmaceutically acceptable carrier are sterile, and are preferably stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration.

Dosage regimens can be adjusted to provide the optimum desired response (e.g., a therapeutic response). For example, a single bolus can be administered, several divided doses can be administered over time, or the dose can be proportionally reduced or increased as indicated by the exigencies of the disease situation.

5 In general, a preferred embodiment of the invention is to administer a suitable daily dose of a therapeutic heteropolymer composition that will be the lowest effective dose to produce a therapeutic effect, for example, mitigation of symptoms. The therapeutic heteropolymer compounds of the invention are preferably administered at a dose per subject per day of at least 2 mg, at least 5 mg, at least 10 mg or at least 20 mg as appropriate minimal  
10 starting dosages. In general, the compound of the effective dose of the composition of the invention can be administered in the range of 50 to 400 micrograms of the compound per kilogram of the subject per day.

A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the effective dose of the pharmaceutical composition required. For example, the  
15 physician or veterinarian could start doses of the compound of the invention employed in the pharmaceutical composition at a level lower than that required in order to achieve the desired therapeutic effect, and increase the dosage with time until the desired effect is achieved.

In another preferred embodiment, the pharmaceutical composition includes also an additional therapeutic agent. Thus in a method of the invention the pharmaceutical  
20 composition can be administered as part of a combination therapy, i.e. in combination with an additional agent or agents. Examples of materials that can be used as combination therapeutics with the heteropolymers for treatment of autoimmune disease and arthritic conditions as additional therapeutic agents include: an antibody or an antibody fragment that can bind specifically to an inflammatory molecule or an unwanted cytokine such as  
25 interleukin-6, interleukin-8, granulocyte macrophage colony stimulating factor, and tumor necrosis factor- $\alpha$ ; an enzyme inhibitor which can be a protein, such as  $\alpha_1$ -antitrypsin, or aprotinin; an enzyme inhibitor which can be a cyclooxygenase inhibitor; an engineered binding protein, for example, an engineered protein that is a protease inhibitor such an engineered inhibitor of kallikrein; an antibacterial agent, which can be an antibiotic such as

amoxicillin, rifampicin, erythromycin; an antiviral agent, which can be a low molecular weight chemical, such as acyclovir; a steroid, for example a corticosteroid, or a sex steroid such as progesterone; a non-steroidal anti-inflammatory agent such as aspirin, ibuprofen, or acetaminophen; an anti-cancer agent such as methotrexate or adriamycin; or a cytokine. An  
5 additional therapeutic agent can be a cytokine, which as used herein includes without limitation agents which are naturally occurring proteins or variants and which function as growth factors, lymphokines, interferons, tumor necrosis factors, angiogenic or antiangiogenic factors, erythropoietins, thrombopoietins, interleukins, maturation factors, chemotactic proteins, or the like. Preferred combination therapeutic agents to be used with  
10 the composition of the invention and which are cytokines include interleukin-4 and interleukin-10. A therapeutic agent to be used with the composition of the invention can be an engineered binding protein, known to one of skill in the art of remodeling a protein that is covalently attached to a virion coat protein by virtue of genetic fusion (Ladner, R. et al., U.S. Patent 5,233,409; Ladner, R. et al., U.S. Patent 5,403,484), and can be made according to  
15 methods known in the art. A protein that binds any of a variety of other targets can be engineered and used in the present invention as a therapeutic agent in combination with a heteropolymer of the invention.

An improvement in the symptoms as a result of such administration is noted by a reduction in edema of one or more joints, by a reduction in inflammation in one or more  
20 joints, or by an increase in mobility in one or more joints. A therapeutically effective dosage preferably reduces joint inflammation and edema and improves mobility by at least about 20%, more preferably by at least about 40%, even more preferably by at least about 60%, and even still more preferably by at least about 80%, relative to untreated subjects.

The therapeutic compounds of the invention can be used to treat symptoms of an  
25 autoimmune disease, a class of disorder which include Hashimoto's thyroiditis; idiopathic myxedema, a severe hypothyroidism; multiple sclerosis, a demyelinating disease marked by patches or hardened tissue in the brain or the spinal cord; myasthenia gravis which is a disease having progressive weakness of muscles caused by autoimmune attack on acetylcholine receptors at neuromuscular junctions; Guillain-Barre syndrome, a polyneuritis;



systemic lupus erythematosus; uveitis; autoimmune oophoritis; chronic immune thrombocytopenic purpura; colitis; diabetes; Grave's disease, which is a form of hypothyroidism; psoriasis; pemphigus vulgaris; and rheumatoid arthritis (RA).

Another embodiment of the invention is a kit for assaying the binding of an analyte to an MHC protein. This embodiment provides: a water-soluble MHC protein which has been recombinantly produced in a non-mammalian cell; a reaction chamber for containing the analyte and the MHC protein; and means for detecting binding of the analyte to the MHC protein. In a preferred embodiment, the MHC protein is produced in an invertebrate or a microbial cell, such as an insect cell or a yeast cell, and so is devoid of bound peptide in the antigen cleft, i.e., the MHC protein is "empty." Means for detecting binding of the analyte to the MHC protein can be radioactive, fluorimetric, chemiluminescent, or colorimetric means known to one of ordinary skill in the art. In a preferred embodiment of the kit, the MHC protein is a class II MHC HLA-DR1 or -DR4 protein. Further, the kit can include also an autoantigenic peptide, such as a CII peptide, or a peptide derived from myelin basic protein, myelin oligodendrite protein, or a peptide from some other protein implicated in an autoimmune disease.

Example 1 below provides the method of preparation of each of the three-amino acid heteropolymers used in the invention, and also provides methods for purification of the MHC class II proteins. Polymerization for preparation of the heteropolymers can be performed using solid state methods, or can be performed in solution. Table 1 shows chemical properties of examples of the three-amino acid heteropolymers, including the molar ratios of the amino acid derivatives used in the polymerization (and the resulting mole percent of each amino acid substituent), and the average molecular weights.

Example 2 includes methods of assay for binding of heteropolymers and peptides to the MHC proteins, for measuring inhibition of binding, and for inhibition of T cell activation response in a cell-cell antigen presentation assay.

Example 3 shows inhibition of binding of random synthetic heteropolymers to recombinant HLA-DR1 and -DR4 molecules by the CII 261-273 epitope peptide, with comparison between the three-amino acid heteropolymers and YEAK. Data are also shown

for binding of the influenza virus hemagglutinin peptide HA 306-318. The heteropolymer that is biotinylated is indicated in bold in the upper left hand corner of each panel, and the competing materials are as indicated for the symbols in each panel of Figs. 1A and 1B. For binding to recombinant class II MHC HLA-DR1 protein, YAK (Fig. 1A, bottom panel) provides greater inhibition of binding of biotinylated YAK than either CII or HA. YEAK is somewhat superior to CII but is not as effective as HA peptide (top panel), and inhibition by YEK is lower than that of each of the natural peptides for inhibition of biotinylated YEK binding. Comparable data for binding to recombinant class II MHC HLA-DR4 protein, shown in Fig. 1B, shows that YAK is again a better inhibitor than the natural peptides; YEAK is not a better inhibitor than CII or HA.

Previous findings suggested that the activity of YEAK (Cop 1) in EAE and MS involves binding to class II MHC molecules within the peptide binding groove, resulting in suppression of autoimmune T cell responses that can be related to MS (Teitelbaum, D., et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:9724; Teitelbaum, D., et al., 1992, *Proc. Natl. Acad. Sci. USA* 89: 137; Fridkis-Hareli, M. et al. 1998, *J. Immunol.* 160:4386, the contents of which are hereby incorporated by reference). In the present invention, the binding of each of YAK and YEK to purified human HLA-DR1 and DR4 molecules has been shown to be stronger than that of YEAK. Further, the binding to RA-associated MHC-DR1 (DRB1\*0101) and DR4 (DRB1\*0401) of determinant CII 261-273 of type II collagen, a candidate autoantigen in RA, was here inhibited by each of YAK, YEK and YEAK. The three-amino acid heteropolymers, in particular those having amino acids lysine, alanine and tyrosine (YAK) and lysine, glutamic acid and tyrosine (YEK), bound purified human HLA-DR1 and -DR4 molecules with high affinity, and competed efficiently for binding with CII peptide. Example 3 shows that the three-amino acid heteropolymers, particularly YAK and YEK, were significantly more potent inhibitors of the MHC molecules than YEAK.

The recombinant empty HLA-DR1 and -DR4 molecules that were here used in assays yielded data for binding that is free from interference due to previously bound endogenous peptides. In contrast, for prior analyses of binding to human HLA-DR1 and DR4 molecules, only 10-20% of the receptor proteins had been available for binding of exogenously supplied

peptide (see, for example, Hammer, J. et al., 1993, *Cell* 74:197-203), resulting in determinations of binding affinities for the heteropolymers that in the present invention are different and more accurate compared to those reports.

The data in Example 4 (Fig. 2 and Fig. 3A, 3B) demonstrate greater inhibition by the three-amino acid random heteropolymers, in comparison to YEAK, of DR1- and DR4-restricted CII-specific T cell response to presentation of the CII antigen. In this in vivo T cell response measuring IL-2 production, YAK provides greatest inhibition. Thus, direct evidence for inhibition of the in vivo CII-specific T cell response by three-amino acid random synthetic heteropolymers as well as the four-amino acid random synthetic heteropolymer is here provided for the first time. This direct evidence is based on criteria from the effects of the presence of heteropolymers in two assays: in vitro competition with other compounds for binding to RA-associated HLA-DR1 and -DR4 molecules, and in vivo inhibition of IL-2 production by DR1- and DR4-restricted T cell hybridomas shown in Example 4.

YEAK binds with high affinity and in a peptide-specific manner to purified MS-associated HLA-DR2 (DRB1\*1501) and rheumatoid arthritis (RA)-associated HLA-DR1 (DRB1\*0101) or HLA-DR4 (DRB1\*0401) molecules. Since YEAK is a mixture of random polypeptides, it may contain different sequences that bind to different HLA proteins; in this case only a fraction out of the whole mixture would be an "active component." Alternatively, the whole mixture may be competent, i.e. all polypeptides binding to any HLA-DR molecule.

Example 5 shows methods for isolating and purifying a fraction of YEAK that bound to recombinant "empty" HLA-DR1, -DR2 and -DR4 molecules, produced so as to have minimal interference from endogenous human peptides. Example 6 shows the distribution of amino acid residues in the fraction of YEAK molecules that bound to the HLA-DR protein molecules. The amino acid composition, HPLC profiles and pool sequence, and immunological recognition of the fraction of the heteropolymer bound to MHC class II protein groove were determined.

Since the average length of the YEAK polypeptides used was 75-80 amino acids, the amino acid sequences comparable to "epitopes" lying in the groove of HLA-DR molecules were likely to be found internally within the polypeptide chains. The presence of the

contiguous amino ends of the polymer that were protruding from the complexes could obscure the sequences of binding motifs to be obtained by microchemical methods of sequence analysis applied directly to the bound YEAKE fraction. Because of this consideration, amino-terminal aminopeptidase treatment in Example 7 of the protruding ends of YEAKE polypeptides was employed to access the internal regions and obtain the binding motif sequences. Since the aminopeptidase trims amino-terminal ends of peptides that protrude from the class II MHC proteins, epitopes that were bound to the groove of the proteins can be protected from aminopeptidase proteolysis.

In Example 8, various 15-mer amino acid peptides were synthesized to resemble sequences of the MHC class II DR-1 and -4 binding motifs obtained from the binding motif sequences found in Example 7. The peptides were tested in Example 9 to determine if they differentially inhibited binding of disease-associated HLA-DR1 (DRB1\*0101) or HLA-DR4 (DRB1\*0401) protein molecules to YEAKE and to the immunodominant epitope of collagen type II (CII) 261-273, a candidate autoantigen in rheumatoid arthritis (RA). Peptide sequences in Example 10 were further tested to obtain those with ability to inhibit significantly the response of HLA-DR1- and -DR4-restricted T cell clones to the CII epitope 261-273 in cell culture in vivo. The findings that certain peptides bind with high specificity and affinity and inhibit T cell activation in Examples 9 and 10 indicate utility of certain of the 15-mer amino acid peptide compounds as therapeutic agents in treatment of autoimmune diseases such as RA and MS.

Methods of use of random synthetic heteropolymers can be the basis of treating other autoimmune diseases which are associated with HLA-DR gene products, by competing with candidate autoantigens for binding to these protein receptor molecules, such that subsequent T cell response to autoantigen is inhibited in vivo. Further, synthetic heteropolymers having one or more additional components, such as amino acid analogs or derivatives added in varying quantities into the polymerization reaction, can be effective inhibitors of a variety of autoimmune T cell responses.

### EXAMPLES

#### Example 1. Methods for preparing heteropolymers and protein reagents

##### Synthesis of heteropolymers and peptides

Heteropolymer YEAk (Cop 1) was prepared as described by polymerization of the N-carboxyanhydrides of L-alanine,  $\gamma$ -benzyl-L-glutamate,  $\epsilon$ ,N-trifluoroacetyl-L-lysine, and L-tyrosine (Teitelbaum, D., et al., 1971, *Eur. J. Immunol.* 1:242). The end product is a mixture of acetate salts of random polypeptides. Heteropolymers EAK, batch SD-1689, MW 8,850; YEA, batch SD-1690, MW 7,600; YAK, batch SD-1691, MW 20,000; and YEK, batch SD-1697, MW 11,050 were synthesized also by polymerization of the N-carboxyanhydride substrates (Fridkis-Hareli, M. et al. 1998, *J. Immunol.* 160:4386, the contents of which are hereby incorporated herein by reference). Heteropolymers can be synthesized also by solid state techniques. Natural peptide sequences influenza hemagglutinin HA peptide 306-318 having the sequence PKYVKQNTLKLAT (SEQ ID NO: 1) and collagen II (CII) peptide 261-273 having the sequence AGFKGEQGPKGEP (SEQ ID NO: 2) were synthesized using solid phase techniques (Barany, G. et al., 1979, *Academic Press*, New York. p. 1) on an Applied Biosystems Peptide Synthesizer (Foster City, CA) and purified by reverse-phase HPLC. For these and other methods used throughout these examples, see also Fridkis-Hareli et al. 1998, *Proc. Natl. Acad. Sci. U.S.* 95:12528-12531, Fridkis-Hareli et al. 1999 *J. Immunol.* 162: 4697-4704, and Fridkis-Hareli et al. 1999, *Internat. Immunol.* 11:635-641, the contents of each of which are hereby incorporated by reference hereby.

The one letter and the three letter amino acid codes (and the amino acid that each represents) are as follows: A means ala (alanine); C means cys (cysteine); D means asp (aspartic acid); E means glu (glutamic acid); F means phe (phenylalanine); G means gly (glycine); H means his (histidine); I means ile (isoleucine); K means lys (lysine); L means leu (leucine); M means met (methionine); N means asn (asparagine); P means pro (proline); Q means gln (glutamine); R means arg (arginine); S means ser (serine); T means thr (threonine); V means val (valine); W means trp (tryptophan); and Y means tyr (tyrosine).

#### Protein expression and purification

Recombinant HLA-DR1 and -DR4 molecules were expressed in *Drosophila* S2 cells as described (Stern, L. et al. 1992, *Cell* 68:465; Dessen, A. et al. 1997, *Immunity* 7:473). Cells were grown in roller bottles at 26°C in Excell 401 medium (Sigma, St. Louis, MO)

supplemented with 0-5% fetal bovine serum (Sigma). Cells were induced by addition of  $\text{CuSO}_4$  to 1 mM final concentration, and cells were incubated an additional 4-5 days.

Immunoaffinity purification of recombinant HLA-DR1 and DR4 was performed as previously reported (Stern, L. et al. 1992, *Cell* 68:465; Dessen, A. et al. 1997, *Immunity*

5 7:473). Supernatant from harvested cells was sequentially passed through Protein A, Protein G and Protein A-LB3.1 columns, followed by elution of the bound HLA-DR with 50 mM 3-cyclohexylamino-1-propane sulfonic acid (CAPS), pH 11.5, and neutralized with 200 mM phosphate (pH 6.0). The eluate was concentrated on a Centriprep 10 membrane (Amicon). Protein concentrations were determined by bicinchoninic acid assay (Pierce Chemical Co.).

#### 10 Peptide labeling

Biotinylation of heteropolymers YEA<sup>K</sup>, EAK, YEA, YAK, YE<sup>K</sup> and HA 306-318 peptide was performed with excess N-hydroxysuccinimide biotin (Sigma) in dimethyl sulfoxide as described (Fridkis-Hareli, M., et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:4872). Unreacted biotin was removed by dialysis (Spectra/Por membrane MWCO 500, Spectrum  
15 Medical Industries, Laguna Hills, CA).

#### Example 2. Methods of assay of inhibition of binding by heteropolymers to MHC class II protein molecules

Two methods were used to evaluate the three-amino acid heteropolymers as competitors of binding to class II MHC HLA-DR1 and -DR4 proteins. In the first assay,  
20 water soluble recombinantly produced proteins were incubated with biotinylated heteropolymers and varying quantities of unlabeled competitor heteropolymers or collagen CII or influenza virus HA peptides. In the second assay, irradiated antigen presenting cells were coincubated with CII peptide and inhibitory heteropolymers, and DR-restricted T cells were then added and assayed for activation by measurement of IL-2 production. These assays  
25 were performed as follows.

#### Class II-peptide-binding assays

The solutions used in this assay are described in Fridkis-Hareli, M. et al. 1998, *J. Immunol.* 160:4386. Assays were performed in 96-well microtiter immunoassay plates (PRO-BIND™, Falcon) which were coated with affinity-purified LB3.1 monoclonal

antibodies, 100  $\mu$ l of 1.0  $\mu$ g/well in PBS (150 mM sodium chloride, 7.5 mM sodium phosphate dibasic, 2.5 mM sodium phosphate monobasic, pH 7.2) by incubation for 18 hrs at 4°C. The wells were then blocked with TBS (137 mM sodium chloride, 25 mM TRIS pH 8.0, 2.7 mM potassium chloride) containing 3% BSA (bovine serum albumin) for 1 hr at 37°C and washed three times with TTBS (TBS with 0.05% Tween-20). Before sample addition, 50  $\mu$ l of TBS containing 1% BSA was added to each well.

Water-soluble HLA-DR1 molecules were recombinantly produced in a heterologous host cell, for example, insect cells infected with recombinant baculoviruses (Stern, L. J. et al., 1992, *Cell* 68:465), specifically in *Drosophila* S2 cells as described supra. Binding analysis was performed by coincubating biotinylated YEAK, YEA, YAK, EAK or YEK (final concentration, 1.5  $\mu$ M) in 50  $\mu$ l of the binding buffer in duplicate with varying concentrations of unlabeled inhibitors (YEA, YAK, EAK, YEK, YEA, CII 261-273 or HA 306-318), and with recombinant water soluble DR molecules (0.15  $\mu$ M) for 40 hr at 37°C at pH 5.0.

#### Detection of peptide-class II complexes

Bound peptide-biotin was detected using streptavidin-conjugated alkaline phosphatase as follows. Plates were washed three times with TTBS and incubated with 100  $\mu$ l of streptavidin-conjugated alkaline phosphatase (1:3000, BioRad, Richmond, VA) for 1 hr at 37°C, followed by addition of *p*-nitrophenyl phosphate in triethanolamine buffer (BioRad). The absorbance at 410 nm was monitored by a microplate reader (model MR4000, Dynatech, Chantilly, VA).

#### T cell hybridomas and antigen presentation assays

The following mouse T cell hybridomas specific for CII were used: DR1-restricted 3.19 and 19.3 clones (Rosloniec, E. F., et al., 1997, *J. Exp. Med.* 185: 1113-1122.), and DR4-restricted 3838 and D3 clones (Andersson, E. C., et al., 1998, *Proc. Natl. Acad. Sc. USA*). APC were L57.23 (L cells transfected with DR1 (Rosloniec, E. F., et al., 1997, *J. Exp. Med.* 185: 1113-1122)), L cells transfected with DR4, and Priess cells (DRB1\*0401/DRB4\*0101) used as indicated in the Figures. T cell stimulation experiments were performed in 96-well microtiter plates in a total volume of 0.2 ml. Irradiated (3000 rad) APC ( $2.5 \times 10^4$ /well) were coincubated with CII 261-273 (40  $\mu$ g/ml) and varying

concentrations of heteropolymers for 2 hr at 37°C, then T cells ( $5 \times 10^4$ /well) were added and incubations were continued for 24 hr at 37°C. Supernatants (30  $\mu$ l) were removed and incubated with IL-2-dependent CTL-L ( $5 \times 10^4$ /well) for 12 hr, followed by labeling with  $^3$ H-thymidine (1  $\mu$ Ci/well) for 12 hr. Plates were harvested and the radioactivity was monitored using a 1450 microbeta Plus liquid scintillation counter (Wallac, Gaithersburg, MD).

*Example 3. Inhibition of binding of random synthetic heteropolymers to recombinant HLA-DR1 and DR4 molecules by peptide CII 261-273: comparison of three-amino acid heteropolymers and YEA indicates that YAK provides greatest inhibition*

An ideal therapeutic agent for an autoimmune disease would have the properties of high affinity and specificity for an MHC class II protein molecule encoded by an allele associated with that particular disease. The extent of the affinity and specificity would enable the agent to compete successfully with a peptide of the autoantigen that binds to the particular MHC class II molecule.

To assess affinity and specificity of binding of various heteropolymers to HLA-DR1 and -DR4 molecules associated with rheumatoid arthritis, heteropolymers consisting of three amino acids that are charged and hydrophobic were assayed and compared to YEA for a variety of kinetic properties associated with MHC class II protein binding. The components, methods of preparation, methods of assay, molar ratios of components, and molecular weights of these heteropolymers used are described in Example 1 and summarized in Table 1. These random heteropolymers are designated in Examples and Figures, using the one-letter amino acid code to indicate their components, as YEA, YEK, YAK and EAK. For ease and consistency of interpretation, the amino acid components are named in full in the claims.

Table 1. Properties of the heteropolymers: molar ratios of the constituents (mole percent for each amino acid) and molecular weight

<u>heteropolymer molar ratios (mole percent for each amino acid)</u>				
<u>amino acid</u>	<u>EAK</u>	<u>YEA</u>	<u>YAK</u>	<u>YEK</u>
tyrosine	0	1.0 (13.7)	1.0 (10.5)	1.0 (16.1)



glutamic acid	1.5 (15)	1.5 (20.6)	0	1.5 (24.2)
alanine	4.8 (48)	4.8 (65.7)	4.8 (50.5)	0
lysine	3.7 (37)	0	3.7 (39.0)	3.7 (59.7)
5 average molecular weight	8,550	7,600	20,000	11,050

To determine whether YAK, YEK, YEA or YEAk compete with the natural sequence RA-associated immunodominant antigen CII 261-273 peptide for binding to HLA-DR1 or  
10 -DR4 molecules, recombinant water-soluble HLA-DR1 and -DR4 proteins produced in insect cells (encoded by DRA/DRB1\*0101 and \*0401, respectively) were employed. The water-soluble proteins made in insect cells are largely free of bound autoantigens or other peptides, in contrast to detergent-soluble proteins isolated from B cells, a substantial molecular fraction of which as purified has bound autoantigens or peptides. Hence data obtained from insect  
15 cell produced proteins are a more accurate indication of actual binding affinities for peptides and heteropolymers (Fridkis-Hareli et al., 1998, *J. Immunol.* 160: 4386, the entire contents of which are hereby incorporated herein by reference).

Competitive binding assays were carried out using biotinylated YEAk, YAK, YEA and YEK, and using as unlabeled inhibitors the heteropolymers YEAk, YAK, YEA, YEK,  
20 and the natural peptides CII 261-273 and HA 306-318 peptide (Fig. 1; EAK was initially found to have low binding and competitive efficiency for HLA-DR1 and -DR4 and was excluded from further analysis). The binding of each of YEAk, YEA and YAK to HLA-DR1 or DR4 molecules was substantially greater than that of CII 261-273 as judged by quantity of CII 261-273 peptide required for 50% inhibition, and was substantially greater  
25 than the binding of YEK. Influenza virus peptide HA 306-318 inhibited the binding of each heteropolymer more efficiently than CII 261-273 (Fig. 1A, B). Inhibition by unlabeled peptides or unlabeled heteropolymers of biotinylated heteropolymer binding to each of DR1 (Fig. 1A) and DR4 (Fig. 1B) by the unlabeled molecule was more efficient for YAK than for YEAk or YEK, as determined by the quantity of unlabeled competitor (shown on the  
30 abscissa) required for a given percent of inhibition. YAK was consistently found to be a

superior inhibitory material than peptide CII 261-273, whereas this was not observed for YEAK, YEK and YEA. The kinetics of inhibition by unlabeled YAK were somewhat superior also to that of the influenza peptide HA306-318.

As shown in this Example and in Fig. 1A and Fig. 1B herein, YEA, YEK, and YAK  
5 heteropolymers were found to bind to the purified human MHC class II HLA-DR1 and -DR4 protein molecules with high affinity. Surprisingly, some of the heteropolymers comprised of three amino acids were found to compete successfully with YEAK for binding to MHC class II proteins. Further, in these in vitro assays of binding, the random three amino acid  
heteropolymers, especially YAK, demonstrated binding to RA-associated HLA-DR1 or -DR4  
10 molecules that was superior to that of the autoantigenic epitope CII 261-273.

Example 4. Inhibition by random heteropolymers of DR1- and DR4-restricted CII-specific T cell response to CII antigen presentation

To determine whether YAK, YEK, YEA or YEAK can inhibit presentation of the rheumatoid arthritis immunodominant epitope CII 261-273 peptide to autoreactive T cells,  
15 CII specific T cell hybridomas which are restricted to HLA-DR1 (3.19 and 19.3) and -DR4 (3838 and D3) were used. Irradiated APC (which can function to bind and present antigens but can not proliferate) were incubated with CII 261-273 and the relevant heteropolymer for 2 hrs, then T cells were added for further 24 hr incubation, and the quantities of IL-2 secreted by the hybridomas in each reaction were measured.

20 YAK, YEK and YEAK were observed to inhibit DR1-restricted T cell response to CII peptide (Fig. 2, top panel). YAK was the most potent inhibitor, and YEA inhibited less efficiently. Both YAK and YEK were substantially more effective inhibitors for DR1 presentation of the CII antigen than YEAK (in two batches of different molecular weights), as YAK at a two- to three-fold lower quantity than YEAK produced comparable inhibition and  
25 YAK achieved a higher end-point of inhibition. Consistent results were obtained with other batches of DR1 APC (Fig. 2, middle and lower panels), showing that YAK has greater inhibitory properties in this assay with immune recognition of the RA-related peptide than YEAK. A similar pattern of activities for these heteropolymers was obtained with DR4-restricted T cells, using as APC either Priess or L fibroblasts transfected with DR4 (Fig.

3).

The ability of DR1 or DR4 protein molecules to present the CII 261-273 antigen to T cells was more greatly diminished in the presence of YAK than of YEK, indicating that the heteropolymer molecules are strong inhibitors of the T cell response, and the relative activities of each of these heteropolymers in inhibiting the process. Thus, based on the T cell activation data, the relative ability of these random heteropolymers to compete with the autoantigenic CII 261-273 peptide is expressed in the following order:

YAK>YEK>YEAK>>YEA.

Example 5. Methods for preparation and quantitation of YEAK bound to HLA-DR1, -DR2 and -DR4 molecules.

YEAK was incubated with water-soluble HLA-DR1, -DR2 or -DR4 molecules at the molar ratio of 1:1 for 40 hr at 37°C. These recombinant "empty" HLA-DR molecules can be stably assembled in the presence of exogenously added antigen, and YEAK can function to promote stabilization and with no interference from endogenous peptides (Fridkis-Hareli, M. et al. 1998. *J. Immunol.* 160:4386). Unbound YEAK was separated from bound YEAK by Centricon ultrafiltration. Bound YEAK was then extracted from the HLA-DR complex by acid treatment (Chicz, R. et al. 1993. *J. Exp. Med.* 178:27) and subjected to amino acid analysis.

For HPLC separation and microsequencing after elution, approximately 5-10% of the YEAK mixtures were fractionated by microbore HPLC using a Zorbax C<sub>18</sub> 1.0 mm reverse-phase column on a Hewlett-Packard 1090 HPLC with 1040 diode array detector. At a flow rate of 54 µl/min, YEAK was eluted with a gradient of 0.055% trifluoroacetic acid (TFA) in acetonitrile (0% at 0 to 10 min, 33% at 73 min and 60% at 105 min). Strategies for peak election, reverse phase separation and Edman microsequencing were performed as in Chiciz, R. et al. 1993. *J. Exp. Med.* 178:27, and Lane, W. et al. 1991. *J. Prot. Chem* 10:151.

To further characterize the bound fraction of YEAK by means of hydrophobicity and size, samples were separated on RP-HPLC using an acetonitrile gradient. Untreated YEAK showed a very broad peak with several smaller peaks, which spread between approximately 40 and 75 min elution time. This elution profile is characteristic of a mixture of random polypeptides and resembles HPLC separations of other batches of YEAK. Similar profiles

were obtained when YEAK was eluted from HLA-DR1, -DR2 or -DR4 molecules, indicating that the bound fraction is similar to the whole original YEAK mixture in its chemical properties.

Example 6. Analysis of YEAK bound to HLA-DR1, -DR2, and -DR4 molecules.

5 At least 95% of the added YEAK heteropolymer molecules was observed in the fraction that was bound to isolated HLA-DR1 and HLA-DR4, and 80% was bound to HLA-DR2 proteins. YEAK that was eluted from the complexes with HLA-DR1, -DR2 and -DR4 molecules showed ratios of the component amino acids Y:E:A:K similar to that of control untreated YEAK. These results indicate that the bound fraction of YEAK reflected the amino  
10 acid composition of the whole mixture and that the YEAK population exhibited little or no preferential binding to different HLA-DR proteins. When YEAK was incubated with an excess of each of HLA-DR1, -DR2 and -DR4 molecules that had been purified from human homozygous EBV-transformed B cell lines, and the complexes were further fractionated by passage through a size-exclusion column, the distribution of eluted material showed that  
15 nearly all of the YEAK was found in the fractions corresponding to the high molecular weight complexes, with less than 10% at the lower molecular weight position of control YEAK, for each of the HLA-DR molecules.

To analyze the sequence of YEAK that bound to each of HLA-DR1, -DR2 and -DR4 molecules, HPLC fractions obtained in Example 5 were pooled within the areas of elution,  
20 and pooled fractions were submitted to automated Edman degradation on a Hewlett-Packard G1005A (Palo Alto, CA) protein sequencer using the manufacturer's Routine 3.5.

For each of the HLA-DR proteins, the results showed that the four amino acid components of YEAK bound to protein were randomly distributed within the sequence according to the input molar ratios of YEAK. Amino acid alanine (A) was found at  
25 significantly higher levels compared to E, Y and K, as expected from the initially higher molar ratio of A in YEAK. There was no sequence specificity or preferential positioning of any of the amino acids of YEAK, indicating that the bound fraction was also random and similar to the entire unfractionated YEAK.

Anti-YEAK polyclonal antibodies were used to determine whether fractions of YEAK  
30 eluted from each of the HLA-DR molecules contained the epitopes found in control untreated

YEAKE. The cross reactivity between YEAKE and various YEAKE fractions was detected by direct ELISA assay using biotinylated anti-YEAKE polyclonal antibodies. YEAKE or fractions were diluted to 0.4 µg/ml and 2.0 µg/ml and 100 µl/well was plated in duplicate on a 96-well microtiter immunoassay plate (PRO-BIND™, Falcon, Lincoln Park, NJ), incubated for 1 hr at 37°C and washed three times with TBS containing 0.05% Tween-20. The wells were then blocked with TBS containing 3% BSA, followed by addition of biotinylated anti-YEAKE antibodies (at a dilution of 1:5000, 100 µl/well). Antibody-ligand complexes were detected using streptavidin-conjugated alkaline phosphatase (at a dilution of 1:3000, BioRad ) and *p*-nitrophenyl phosphate in triethanolamine buffer (BioRad; Hercules, CA). The absorbance at 410 nm was monitored by a microplate reader (Dynatech MR4000).

The antibody binding assays showed that all the fractions were similarly recognized by anti-YEAKE antibodies, suggesting that these bound heteropolymer fractions shared similar or identical epitopes with each other and with control YEAKE.

Example 7. *Characterization of binding motifs of YEAKE by removal of protruding amino termini of YEAKE bound to HLA-DR1, -DR2 or -DR4 molecules with aminopeptidase I.*

The sequences of the first 20 to 25 N-termini amino acids observed in Example 6 represent the sequences that protrude from beyond the HLA-DR molecules, so are not a source of information regarding the actual binding motif(s) of YEAKE bound within the functional epitope-specific groove. To obtain the amino acid sequence of the portion of the YEAKE molecule bound within the MHC class II protein and so protected by this protein, YEAKE (1mM) was initially incubated with each of the HLA-DR molecules (100 µm) in a volume of 10 µl at the molar ratio of 10 YEAKE:1 HLA-DR, in PBS for 40 hours at 37°C. Aminopeptidase I, a metalloprotein isolated from *Streptomyces griseus* (Spungin A. et al. 1989. *J. Biochem.* 183:471; available from Sigma Chemicals, St. Louis, MO), was added to the reaction in a volume of 2 µl containing 2 units for the last 18 hr of incubation, in order to remove amino-terminal ends of YEAKE polypeptides protruding from the HLA-DR molecules, and to digest remaining unbound YEAKE (Mouritsen, S. et al. 1992. *J. Immunol.* 148:1987; Larsen, S. L. et al. 1996. *J. Exp. Med.* 184:183). Subsequent digestions of heteropolymer with aminopeptidase was performed in volumes scaled up by a factor of twenty-four fold, for example, 300 µl of heteropolymer digested with 60 µl of

aminopeptidase. Samples were spin-concentrated to a final volume of approximately 100  $\mu$ l using Centricon 10 ultrafiltration devices.

The YEAH-HLA-DR complexes and the unbound YEAH were analyzed by SDS-PAGE. SDS-PAGE was carried out with the NOVEX mini cell electrophoresis system.

- 5 Separation gel was 10% in acrylamide and stacking gel was 5%. HLA-DR1-YEAH complexes were run under nonreducing conditions for 1 hr at 200 V, stained with Coomassie Brilliant Blue, fixed for 3 hr in 10% methanol/10% acetic acid and dried on Cellophane paper (BioRad) at 25°C. The YEAH-HLA-DR complexes were found to be resistant to SDS-induced dissociation, forming higher molecular weight complexes with HLA-DR1  $\alpha\beta$
- 10 heterodimers, and were observed as numerous bands on the polyacrylamide gel with molecular weights greater than the molecular weight protein standard of 50 kD, showing that the YEAH-DR complexes were protected. Aminopeptidase I treatment resulted in unbound YEAH appearing as a smear in the lower part of the gel, showing that it was completely digested by the enzyme.
- 15 To obtain the sequence of the binding motifs, fractions containing the peaks of protected YEAH were selected in the region between approximately 40 and 75 min elution time for each class of HLA-DR complex. Bound YEAH absent the protruding N-termini was eluted from HLA-DR by addition of acetic acid (10%) and incubation at 70°C for 15 min, followed by ultrafiltration and vacuum concentration in a SpeedVac (Savant Instruments,
- 20 Farmingdale, NY; Fridkis-Hareli, M. et al. 1995. *Cell. Immunol.* 163:229). The sequence data (Table 2) show that for peptides bound to HLA-DR1, significantly higher levels of the E residue were found at the first and second cycles, higher levels of K residue were found at the second and third cycles, and higher levels of Y residue were found at the third to fifth cycle (presumably at the position corresponding approximately to the P1 of the bound peptide site
- 25 within the MHC class II groove). The amino acid residue obtained from position 3 from the Edman degradation method corresponds to the P1 anchor position of the MHC class II peptide binding groove, since in the structure of the HA 306-318 complex with HLA-DR1, the P-2 amino acid residue is at the flush end of the groove and the P1 position is the third amino acid, that is, Y308, in a deep pocket (Stern, L. et al., *Nature (Lond.)* 368:215). These
- 30 data are in contrast to the random patterns of the sequences found in untreated YEAH, which

showed no sequence specificity or preferential positioning within the MHC class II groove of any of the four amino acids that comprise YEAK.

For HLA-DR2, both Y and A residue levels were enriched at cycle 3 (Table 2). No sequence specificity or preferential positioning was observed for positions corresponding to anchor positions following P1 (at positions in the sequence that correspond to the P4, P6 or P9 of HLA-DR1 or -DR4; P4, P7 of DR2b molecules). In all the samples the levels of A were higher than those of E, Y and K, a finding which was expected and corresponds to the higher molar ratio of A in YEAK. For each of the HLA-DR-1 and -4 molecules, Y was found at the position corresponding to the first anchor position (the third residue in the sequence analysis), followed by A in the positions corresponding to the subsequent pockets. In the YEAK bound to HLA-DR2 also, Y was enriched at the position corresponding to P1. At the first cycle position corresponding to the P-2 position, E was enriched, and at the next adjacent position corresponding to P-1, K was enriched. These residues can contribute to the stable interactions of YEAK with the HLA-DR molecules and the interaction of this complex with the T cell receptor (TCR).

These results indicate that YEAK contains class II MHC binding motifs. Without being bound by any particular theory, it is shown by these data that YEAK, bound to the antigen groove of HLA-DR molecules, can act either as a blocking peptide or as an antagonist or partial agonist, resulting in suppression of autoimmune T cell responses or anergy, or both. The binding motif sequences are useful for mapping the T cell epitopes, and for design of novel agents for the treatment of autoimmune diseases, such as MS and RA in humans.

*Example 8. Synthesis of peptides having binding motifs for HLA-DR1 and -DR4 molecules*

Examples above show that the YEAK heteropolymer bound to purified human HLA-DR molecules within the peptide binding groove and inhibited the binding of HA 306-318

Table 2. Binding motif sequences of YEAK bound to HLA-DR1, -DR2 and -DR4 molecules

HLA-DR	<u>relative amino acid positions</u>						
	-2	-1	1	4	6	7	9

DRB1*0101	DR-1	E	K	Y	A	A	A	A
DRB1*0401	DR-4	E	K	Y	A	A	A	A
DRB1*1501	DR-2	E	K	Y,A	A	A	A	A

5

peptide, a high affinity epitope of influenza virus, to both HLA-DR1 (DRB1\*0101) and -DR4 (DRB1\*0401) molecules. Further, random heteropolymers composed of only three amino acids (EAK, YEA, YAK and YEK) bound to purified HLA-DR1, -DR2 and -DR4 molecules and competed with CII 261-273 for binding to RA-associated HLA-DR1 (DRB1\*0101) and -DR4 (DRB1\*0401) protein molecules, and inhibited CII-reactive T cell clones. The fraction of YEA that bound to the protein was isolated from complexes with recombinant "empty" HLA-DR molecules produced in insect cells, and binding motifs were resolved by aminopeptidase I treatment of the YEA that bound to the complex in the major groove of HLA-DR1 or -DR4 molecules. Subsequent pool sequencing of eluted peptides showed increased in levels of E at the first and second cycles, of K at the second and third cycles, and of Y (at P1 of the bound peptide) at the third to fifth cycle of the amino acid residues, regardless of the HLA-DR molecule employed.

In this Example, peptides of defined sequence and 15 residue length were synthesized using the sequences of the binding motifs summarized in Table 2. These peptides were analyzed in the Examples below for affinity and specificity of binding to MHC class II HLA DR protein molecules and for ability to inhibit binding of competitor molecules and ability to inhibit T cell responses, functional properties appropriate to a novel therapeutic composition for an autoimmune disease.

Peptides shown in Table 3 were synthesized using solid phase techniques (Barany, G. et al., 1979. *The Peptides*, E. Gross et al., eds. (New York, NY: Academic Press) on an Applied Biosystems Peptide Synthesizer, and were purified by reversed-phase HPLC. Peptide sequences included HA 306-318, PKYVKQNTLKLAT (SEQ ID NO: 1), MW 1718; CII 261-273, AGFKGEQGPKGEP (SEQ ID NO: 2), MW 1516; and HA 306-318 bracketed by alanines at N- and C-terminals, APKYVKQNTLKLATA (SEQ ID NO: 4). For comparison, the cII 261-273 peptide, bracketed by alanines at N- and C-terminals, AGFKGEQGPKGEP (SEQ ID NO: 3), can be synthesized. Peptides were also synthesized



on a 1  $\mu$ mole scale using the Multipin Peptide Synthesis System (Chiron Technologies, Raleigh, NC). Peptides were synthesized as 15-mers with free amino groups at the N-terminus and free carboxyl groups at the C-terminus, and with biotin linked to the N-terminus by the spacer SGSG and having a free carboxyl group at the C-terminus. Peptide  
5 synthesis was monitored by including two standard peptide sequences as controls, which were subjected to HPLC and mass spectroscopy analysis. HA 306-318 peptide was also used as a positive control for binding experiments. Pin peptides were lyophilized and resuspended at a concentration of 2 mg/ml in dimethyl sulfoxide (DMSO). Under these conditions, the majority of peptides were completely solubilized. Biotinylation was  
10 performed with excess N-hydroxysuccinimide biotin (Sigma, St. Louis, MO) in DMSO as described (Fridkis-Hareli et al., 1994. *Proc. Natl. Acad. Sci., U.S.A.* 91:4872-4876). Unreacted biotin was removed by dialysis (Spectra/Por® membrane MWCO 500, Spectrum Medical Industries, Houston, TX).

The 15-mer peptides (SEQ ID NOs: 5-36; see Table 3) synthesized based on the  
15 motifs for binding of YEAK to the groove of HLA-DR1 and -DR4 molecules contained various combinations of E, K and A at the N-terminus for most of the peptides, followed by Y at the position corresponding to P1 (shown in bold), and then A in the subsequent binding pockets. The sequences fall into three different groups according to these positions in the consensus (Table 3). Peptides in group I had K at the position corresponding to P8 and Y  
20 at the position corresponding to P1 (in bold in Table 3). A reference peptide in this set with lysine (K) at the position corresponding to P8 to increase solubility and alanine (A) at all other residues had previously been synthesized (SEQ ID NO: 5; Jardetzky, T. S., et al. 1990. *EMBO J.* 9, 1797-1803). Peptides in group II had Y at the position corresponding to P1, however had A at the position corresponding to P8. Peptides in group III had amino  
25 acid tyrosine (Y) shifted one or two residues with respect to that in HA 306-318 peptide. Peptides in all groups contained one or more glutamic acid (E) and/or lysine (K) residues, as was observed in the binding motifs supra, and to enhance solubility. Both N-terminal biotinylated and unlabeled sets of peptides were synthesized for these studies.

30 Table 3. Groups of synthetic peptides and consensus positions.

group	SEQ ID NO	peptide sequence	amino acid consensus positions
Control	4	APKYVKQNTLKLATA	A(HA 306-318)A
5			
I.	5	AAAYAAAAAAAAKAAAA	P1Y, P8K
	6	AEKYAAAAAAAAKAAAA	
	7	AKEYAAAAAAAAKAAAA	
	8	AKKYAAAAAAAAKAAAA	
10	9	AEAYAAAAAAAAKAAAA	
	10	KEAYAAAAAAAAKAAAA	
	11	AEEYAAAAAAAAKAAAA	
	12	AAEYAAAAAAAAKAAAA	
	13	EKAYAAAAAAAAKAAAA	
15	14	AAKYAAAAAAAAKAAAA	
	15	AAKYAEAAAAAAAAKAAAA	
	16	EAAYAAAAAAAAKAAAA	
	17	EKKYAAAAAAAAKAAAA	
	18	EAKYAAAAAAAAKAAAA	
20			
II.	19	AEKYAAAAAAAAAAAAA	P1Y, P8A
	20	AKEYAAAAAAAAAAAAA	
	21	AKKYAAAAAAAAAAAAA	
	22	AKKYAEAAAAAAAAAAAA	
25	23	AEAYKAAAAAAAAAAAAA	
	24	KEAYAAAAAAAAAAAAA	
	25	AEEYKAAAAAAAAAAAAA	
	26	AAEYKAAAAAAAAAAAAA	
	27	EKAYAAAAAAAAAAAAA	
30	28	AAKYAAAAAAAAAAAAA	
	29	AAKYAEAAAAAAAAAAAA	
	30	EKKYAAAAAAAAAAAAA	
	31	EAKYAAAAAAAAAAAAA	
35			
III.	32	AEYAKAAAAAAAAAAAAA	P1A, P8A
	33	AEKAYAAAAAAAAAAAAA	
	34	EKYAAAAAAAAAAAAA	
	35	AYKAEAAAAAAAAAAAAA	
	36	AKYAEAAAAAAAAAAAAA	
40			

Example 9. Inhibition of YEAK and antigen binding to HLA-DR molecules by the synthetic

### 15-mer peptides

To examine whether the synthetic peptides can compete successfully for binding to HLA-DR1 and -DR4 with YEAKE or with the high affinity HA 306-318 peptide, competitive binding assays were carried out with both biotinylated YEAKE or HA 306-318 (bracketed by alanines) and unlabeled inhibitors (YEAKE and the synthetic 15-mer peptides). Kinetic studies indicated that biotinylated YEAKE inhibited binding of unlabeled YEAKE and of HA 306-318 (peptide SEQ ID NO: 4) to recombinant HLA-DR1 better than of peptides in groups I-III. However, several peptides containing K at the position corresponding to P8 (group I) were better inhibitors than peptides that were similar but having A at the position corresponding to P8 (from groups II and III of Table 3). In contrast, the binding of biotinylated YEAKE to HLA-DR4 molecules was efficiently inhibited by many of the peptides in groups I-III, but the binding of biotinylated HA 306-318 to HLA-DR4 was better inhibited by YEAKE than by HA 306-318 or by the 15-mer peptides.

To further characterize the relative affinity of the synthetic 15-mer peptides to compete with each of YEAKE, HA 306-318 or CII 261-273 for binding to HLA-DR1, -DR2 and -DR4 molecules, competitive binding assays were carried out with biotinylated Multipin peptides and the three unlabeled inhibitors. The binding of the majority of the

Table 4. Affinity of selected YEAKE-related peptides for HLA-DR1 (DRB1\*0101) molecules determined by competition with biotinylated competitors HA306-318 and YEAKE ( $\mu\text{M}$ )

SEQ ID NO	peptide sequence	HA 306-318	YEAKE
4	APKYVKQNTLKLATA	13.0	3.3
7	AKEYAAAAAAKAAAA	19.0	
12	AAEYAAAAAAKAAAA	47.0	
15	AAKYAEAAAAKAAAA	42.0	16.0
18	EAKYAAAAAAKAAAA	33.0	
	YEAKE	10.0	8.0

peptides in groups I-III to both HLA-DR1 and HLA-DR4 was inhibited by unlabeled YEAKE, HA 306-318 (SEQ ID NO: 4) or CII 261-273 (SEQ ID NO: 2), however, less

efficiently than the binding of HA 306-318 (SEQ ID NO: 4). Some of the peptides however showed higher affinity for the HLA proteins than did YEAK, HA306-318, or CII 261-273.

All peptides were further tested for ability to inhibit CII-specific T cell responses.

5 Example 10. Inhibition of HLA-DR1- and -DR4-restricted CII-specific T cell responses by the 15-mer synthetic peptides

To determine whether the synthetic peptides could also inhibit presentation of the CII 261-273 peptide to autoreactive T cells, complexes of APC and peptides were tested with CII-specific T cell hybridomas restricted to HLA-DR1 (3.19 and 19.3) and HLA-DR4 (3838  
10 and D3) as described in Examples supra. Irradiated APC were incubated with CII 261-273 and of each of the relevant peptides for 2 hrs, T cells were added and the incubation continued for 24 hrs, and supernatants were tested to determine quantities of IL-2 secretion by these hybridomas as a measure of T cell activation.

Peptides SEQ ID NOs: 15 and 26 were observed to be the most potent inhibitors of  
15 HLA-DR1-restricted T cells, using L fibroblasts transfected with HLA-DR1 as APC for the CII peptide. Peptides 15, 20, 26 and 27 inhibited responses to 19.3 T cells essentially 100%, to levels of inhibition greater than observed with HA 306-318. For 3.19 cells, inhibition by peptide #26 was equivalent to that of HA 306-318. YEAK had little effect on this CII-specific T cell response (inhibition less than 20%). HA 306-318 (peptide SEQ ID  
20 NO: 4) inhibited both DR1 3.19 and 19.3 T cell clones very efficiently (over 95% and 98% for 19.3 and 3.19 cells, respectively). These data show that peptides of SEQ ID NO: 15, 20, 26, and 27 were as good or better inhibitors of T cell response than the reference influenza virus hemagglutinin peptide HA 306-318.

For HLA-DR4-restricted T cells, using L fibroblasts transfected with HLA-DR4 as  
25 APC, the following pattern of activity was obtained: peptides SEQ ID NOs: 6, 11, 16, 17, 22, 23, 27, 28 and 33 were good inhibitors of the DR4 3838 T cell clone, whereas the D3 clone was inhibited best by peptides SEQ ID NOs: 8, 15, 16, 18 and 27. These peptides produced levels of inhibition of over 80% for the D3 and 3838 cells. YEAK had only a minimal effect on the CII-specific T cell response, consistently giving less than 20%  
30 inhibition. HA 306-318 (SEQ ID NO: 4) inhibited both DR4 3838 and D3 T cell clones

less efficiently (less than 60% inhibition) than it inhibited the DR1 3.19 and 19.3 clones. These data show that peptides of SEQ ID NO: 8, 15, 16, 18, and 27 were significantly better inhibitors of T cell response than the reference influenza virus hemagglutinin peptide HA 306-318. Peptides of SEQ ID NO: 15 and 27 were high level inhibitors both of HLA-DR-1- and -DR-4-restricted CII-specific T cells.

Table 5. Affinity of selected YEAK-related peptides for HLA-DR4 (DRB1\*0401) molecules determined by competition with biotinylated competitors HA306-318 and YEAK ( $\mu$ M)

SEQ ID NO	peptide sequence	HA 306-318	YEAK
4	APKYVKQNTLKLATA	26.0	8.2
5	AAAYAAAAAAKAAAA	7.0	
15 6	AEKYAAAAAAKAAAA	6.5	
7	AKEYAAAAAAKAAAA	4.5	
10	KEAYAAAAAAKAAAA	4.5	
11	AEEYAAAAAAKAAAA	2.0	
12	AAEYAAAAAAKAAAA	3.2	1.6
20 13	EKAYAAAAAAKAAAA	3.3	
14	AAKYEAAAAAAKAAAA	4.0	
15	AAKYAEAAAAKAAAA	1.8	<1.0
16	EAAYAAAAAAKAAAA	5.0	
17	EKKYAAAAAAKAAAA	1.8	
25 18	EAKYAAAAAAKAAAA	4.4	3.0
21	AKKYEAAAAAAAAAAA	2.2	
26	AAEYKAAAAAAAAAAA	1.8	
28	AAKYEAAAAAAAAAAA	1.2	
29	AAKYAEAAAAAAAAAAA	1.2	
30 32	AEYAKAAAAAAAAAAA	3.0	
33	AEKAYAAAAAAAAAAA	<1.0	
35	AYKAEAAAAAAAAAAA	1.3	
36	AKYAEAAAAAAAAAAA	3.0	
	YEAK	2.5	20.0

The data in these examples, performed with each peptide at least in duplicate, show that of 32 unique synthetic peptides, several inhibited binding of HA 306-318 and YEAK to recombinant HLA-DR1 and -DR4 molecules. Peptides which inhibited binding of HA 306-

318 or YEAK to HLA-DR1 or -DR4 molecules contained Y at the P1 position. The presence of E, A and K in various combinations on the N-terminal side of P1 did not seem to influence the affinity of the binding. Of the subsequent residues, K at P8 was important for inhibition of HA 306-318 but not of YEAK binding to HLA-DR1. In contrast to HLA-DR1, a larger  
5 number of peptides inhibited binding of both HA 306-318 and YEAK to HLA-DR4 molecules. These peptides contained Y at the position corresponding to P1 and either K or A at the position corresponding to P8, with no preferences for specific amino acids at other positions. The affinity of the HA 306-318 for recombinant HLA-DR4 was lower, and that of YEAK higher, than for HLA-DR1 molecules, similarly to the case observed with HLA-DR1 and -DR4  
10 molecules purified from human blood. The binding of some of the biotinylated peptides to either HLA-DR1 or -DR4 was inhibited by CII 261-273, as well as by HA 306-318 and YEAK, showing that these peptides may compete for presentation to CII-reactive T cells, similar to the whole YEAK mixture. Peptides with an affinity close to or higher than that of the reference natural peptides or the YEAK-mixture are listed in Tables 4 and 5, for HLA-DR1  
15 and HLA-DR4, respectively.

Several of the 15-mer peptides inhibited type II collagen-specific T cell clones. These peptides all had Y at the position corresponding to P1 and either K or A at the position corresponding to P8, with no other specific patterns. Examples here show the strong inhibition by several random heteropolymers composed of three amino acids selected from the group  
20 consisting of Y, E, A and K. These heteropolymers, especially YAK, competed with CII 261-273 for binding to RA-associated HLA-DR1 and -DR4 molecules, and inhibited CII-reactive T cell clones. Further, peptide SEQ ID NO: 8, which includes the direct sequence YAK, inhibited type II collagen-reactive T cells better than YEAK, indicating that a peptide of approximately 15 amino acids in length having the single sequence YAK can substitute for the  
25 mixture of random polypeptides found in the heteropolymer poly(Y,A,K).

The results of the Examples that are the embodiments of the invention, that the individual components of Y, E, A and K or peptides have sequences that correspond to binding motifs for anchor positions fitting the particular HLA-DR molecule (Y at the position corresponding to P1) can act as effective therapeutic agents for autoimmune  
30 diseases, substituting for a mixture of random polypeptides. A pharmaceutical

composition comprising a pure synthetic short polypeptide of identified sequence can have fewer side effects when administered to a subject than a mixture of polypeptides of random sequence. Further, a particular peptide sequences that is effective in binding to an HLA-DR molecule can be embedded into a longer sequence, for example, containing direct  
5 repeats of the peptide sequence or other molecules such as amino acid analogs, to increase stability in vivo or to impart other desirable properties. A pharmaceutical composition comprising a pure synthetic longer identified sequence can be most effective in having greatest efficacy and least toxicity.

What is claimed is:

1. A synthetic peptide having an amino acid sequence comprising at least three residues selected from the group of amino acids consisting of aromatic acids, negatively charged amino acids, positively charged amino acids, and aliphatic amino acids,  
5 the synthetic peptide being at least seven amino acid residues in length and capable of binding to an MHC class II protein associated with an autoimmune disease.
2. A composition according to claim 1, wherein the aromatic amino acid is selected from the group consisting of tyrosine (Y), valine (V), and phenylalanine (F).  
10
- 3 A composition according to claim 2, wherein the positively charged amino acid is lysine (K) and the sequence is selected from the group consisting of lysine-tyrosine (KY), lysine-valine (KV), and lysine-phenylalanine (KF).
- 15 4. A composition according to claim 3, wherein the negatively charged amino acid is glutamic acid (E), and the sequence is selected from the group consisting of glutamic acid-lysine-tyrosine (EKY), glutamic acid-lysine-valine (EKV), and glutamic acid-lysine-phenylalanine (EKF).
- 20 5. A composition according to claim 4, wherein the amino acid which is aliphatic is alanine (A), and the sequence is selected from the group consisting of glutamic acid-lysine-tyrosine-alanine (EKYA), glutamic acid-lysine-valine-alanine (EKVA), and glutamic acid-lysine-phenylalanine-alanine (EKFA).
- 25 6. A composition according to claim 5 wherein the sequence further comprises an amino-terminal alanine, and the sequence is selected from the group consisting of alanine-glutamic acid-lysine-tyrosine-alanine (AEKYA), alanine-glutamic acid-lysine-valine-alanine (AEKVA), and alanine-glutamic acid-lysine-phenylalanine-alanine (AEKFA).



7. A composition according to claim 6, wherein the autoimmune disease is an arthritic condition.

8. A composition according to claim 7, wherein the arthritic condition is  
5 rheumatoid arthritis.

9. A composition according to claim 2, wherein the aliphatic amino acid is alanine, and the amino acid sequence is selected from the group consisting of: lysine-glutamic acid-tyrosine-alanine (KEYA), lysine-tyrosine-alanine-glutamic acid (KYAE),  
10 lysine-glutamic acid-valine-alanine (KEVA), lysine-valine-alanine-glutamic acid (KVAE), lysine-glutamic acid-phenylalanine-alanine (KEFA), and lysine-phenylalanine-alanine-glutamic acid (KFAE).

10. A composition according to claim 3, wherein the aliphatic amino acid is  
15 alanine (A) and the amino acid sequence is selected from the group consisting of lysine-tyrosine-alanine-alanine (KYAA) or lysine-lysine-tyrosine-alanine (KKYA), lysine-valine-alanine-alanine (KVAA) or lysine-lysine-valine-alanine (KKVA), lysine-phenylalanine-alanine-alanine (KFAA), and lysine-lysine-phenylalanine-alanine (KKFA).

20 11. A composition according to claim 3, wherein the peptide further comprises two alanine residues, and the sequence is selected from the group consisting of alanine-lysine-tyrosine-alanine-glutamic acid (AKYAE), glutamic acid-alanine-lysine-tyrosine-alanine (EAKYA), alanine-lysine-valine-alanine-glutamic acid (AKVAE); and glutamic acid-alanine-lysine-valine-alanine (EAKVA), and alanine-lysine-phenylalanine-  
25 alanine-glutamic acid (AKFAE); and glutamic acid-alanine-lysine-phenylalanine-alanine (EAKFA).

12. A composition according to claim 1 wherein the peptide is 7-100 amino acid residues in length.

13. A composition according to claim 1, formulated as a unitary dosage in a pharmaceutically acceptable carrier.
14. A composition according to claim 1, which is substantially pure.
- 5 15. A composition according to claim 1, having greater affinity for the antigen binding groove of an MHC class II protein associated with the autoimmune disease than a type II collagen 261-273 peptide.
- 10 16. A composition which is a synthetic peptide having therapeutic activity in a subject suffering from an autoimmune disease, wherein the peptide has an amino acid sequence having at least one of each of amino acids glutamic acid, lysine, and alanine and an amino acid selected from the group consisting of tyrosine, valine, and phenylalanine.
- 15 17. A composition according to claim 16, wherein the peptide is 7-100 amino acids in length.
18. A composition according to claim 17, wherein the peptide is 7-50 amino acids in length.
- 20 19. A composition according to claim 18, wherein the peptide is 7-25 amino acids in length.
20. A composition according to claim 19, wherein the peptide is 7-15 amino acids in length.
- 25 21. A composition according to claim 16, comprising amino acid analogs at residue locations and in amounts sufficient to inhibit protease degradation of the peptide in the subject.

22. An isolated peptide composition having a sequence selected from the group consisting of: AKEYAAAAAAKAAAA (SEQ ID NO: 7), AAEYAAAAAAKAAAA (SEQ ID NO: 12), AAKYAEAAAAKAAAA (SEQ ID NO: 15), and EAKYAAAAAAKAAAA (SEQ ID NO: 18).

5

23. An isolated peptide according to any of the peptides of claim 22, in which the tyrosine (Y) has been substituted by a valine (F) or a phenylalanine (F).

24. An isolated peptide composition having a sequence selected from the group consisting of: AEKYAAAAAAKAAAA (SEQ ID NO:6), AKEYAAAAAAKAAAA (SEQ ID NO: 7), K EAYAAAAAAKAAAA (SEQ ID NO: 10), AEEYAAAAAAKAAAA (SEQ ID NO: 11), AAEYAAAAAAKAAAA (SEQ ID NO: 12), EKAYAAAAAAKAAAA (SEQ ID NO: 13), AAKYEAAAAAAKAAAA (SEQ ID NO: 14), AAKYAEAAAAKAAAA (SEQ ID NO: 15), EAAYAAAAAAKAAAA (SEQ ID NO: 16), EKKYAAAAAAKAAAA (SEQ ID NO: 17), EAKYAAAAAAKAAAA (SEQ ID NO: 18), AKKYEAAAAAAAAAAAA (SEQ ID NO: 21), AAEYKAAAAAAAAAAAA (SEQ ID NO: 26), AAKYEAAAAAAAAAAAA (SEQ ID NO: 28), AAKYAEAAAAAAAAAAAA (SEQ ID NO: 29), AEYAKAAAAAAAAAAAA (SEQ ID NO: 32), AEKAYAAAAAAAAAAAA (SEQ ID NO: 33), AYKAEAAAAAAAAAAAA (SEQ ID NO: 35), and AKYAEAAAAAAAAAAAA (SEQ ID NO: 36), the peptide having high affinity for an MHC class II protein.

15

20

25. An isolated peptide according to any of the sequences of claim 24, in which the tyrosine (Y) has been substituted by a valine (F) or a phenylalanine (F).

25

26. An isolated peptide composition having an amino acid sequence capable of inhibiting an immune response in a subject to an autoantigen, wherein a position in the amino acid sequence of the peptide that corresponds to an antigen binding pocket in a peptide binding groove of an MHC class II DR protein is identified as a particular amino

acid.

27. An isolated peptide composition according to claim 26, wherein the autoantigen is associated with a condition selected from the group consisting of multiple sclerosis and arthritis.

28. An isolated peptide composition according to claim 26, wherein the MHC class II protein is selected from the group consisting of an MHC class II HLA-DR1 protein, and an MHC class II HLA-DR4 protein.

29. An isolated peptide composition according to claim 26, wherein the MHC class II protein is an MHC class II HLA-DR2 protein.

30. An isolated peptide composition according to claim 26, wherein the amino acid residue in the position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is selected from the group consisting of a tyrosine, a valine, and a phenylalanine.

31. An isolated peptide composition according to claim 26, wherein the amino acid residue in a first amino acid position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is alanine.

32. An isolated peptide composition according to claim 26, wherein the amino acid residue located eight residues beyond the first amino acid position of the sequence that corresponds to the P1 pocket in the MHC class II peptide binding groove is selected from the group consisting of lysine and alanine residues.

33. A pharmaceutical preparation comprising a first peptide sequence and a second peptide sequence, wherein the preparation is a mixture of a first peptide and a

second peptide of different amino acid sequences both according to claim 26 in a pharmaceutically acceptable carrier, the first sequence having in addition a lysine residue and the second sequence having an alanine residue at the amino acid position corresponding to eight residues beyond the amino acid corresponding to the P1 pocket in the MHC class II peptide binding groove.

34. A method for obtaining an MHC class II binding motif amino acid sequence in a mixture of synthetic peptide heteropolymers having therapeutic activity in a subject, comprising:

- 10 (a) binding the mixture of synthetic heteropolymers to MHC class II protein molecules to form a heteropolymer-MHC protein complexes;
- (b) removing by peptidase enzyme digestion the amino terminal amino acid residues of the heteropolymers protruding from the heteropolymer-MHC protein complex to align amino termini of the heteropolymers to the edge of the MHC protein
- 15 complexes; and
- (c) eluting the aligned heteropolymers from the MHC protein by dissociating the complexes to release the amino terminal aligned heteropolymers having the binding motif.

20 35. A method according to claim 34 wherein an additional step (d) comprises: determining the amino terminal sequence of the aligned heteropolymers, to identify the binding motif.

36. A method according to claim 35 wherein an additional step (e)

25 comprises: comparing the amino terminal sequence of the aligned heteropolymers to the amino acid sequence of the synthetic heteropolymer composition.

37. A method according to claim 34, wherein the MHC class II protein is associated with an autoimmune disease.

38. A method according to claim 37, wherein the autoimmune disease is an arthritic condition or a demyelinating condition.

39. A method according to claim 35, wherein an additional step (e)  
5 comprises: synthesizing a plurality of peptide preparations, each peptide preparation having a binding motif amino acid sequence.

40. A method according to claim 39 wherein an additional step (f) comprises:  
determining the affinity of each of the synthesized peptides for the MHC class II protein.

10

93417